

Bette Korber is a Laboratory Fellow at the Los Alamos National Laboratory and an external professor at the Santa Fe Institute. She leads the HIV sequence and immunology database project at Los Alamos, providing a curated collection of published HIV sequence and immune response data gathered from around the globe; the data can be accessed through web search interfaces that integrate sequence diversity and immune response data, and can be evaluated using an extensive set of web based bioinformatics tools designed to assist HIV researchers. In the 1990s, she began to work on the design of artificial ancestral or consensus HIV proteins for vaccine antigens with the intent of eliciting more cross-reactive immune responses. Building on these earlier concepts, she developed a machine learning strategy to design HIV polyvalent vaccines that maximize coverage of T cell epitopes. She and her team demonstrated the importance of phylogenetic corrections in defining viral amino acid mutational patterns that are associated with particular phenotypes, and applied these strategies to understanding how the virus can evade the immune response. Her group has focused on elaborating the evolutionary events that typify viral transmission and new infections, and characterizing the role of the human immune response in viral evolution. Currently she is studying the co-evolution of antibodies and HIV during the course of an HIV infection, as a basis for novel B cell-based vaccine designs, through the NIH funded CHAVI-ID project. She is also working on a CAVD project funded through the GATES foundation, to better understand the consequences of immune responses and selection on driving HIV diversity at population level.